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| **Table 1. Summary of Top Differentially Expressed Genes** | | | | | | | | |
| **LH** | | | **DMH** | | | **ARC** | | |
| **gene** | **log2FC** | **eFDR** | **gene** | **log2FC** | **eFDR** | **gene** | **log2FC** | **eFDR** |
| *Npvf* | -2.13038 | 0.0438 | *Gabpb2* | -2.14412 | 0.0014 | *Irx2* | 1.978426 | 0.0024 |
| *Hmx2* | -1.93924 | 0.013 | *Izumo1* | -1.78528 | 0.0114 | *Micall1* | 1.660793 | 0.0142 |
| *Mc3r* | -1.93781 | 0.0004 | *Cd68* | -1.76592 | 0.0004 | *Aqp1* | -1.65694 | 0.024 |
| *Ghrh* | -1.93195 | 0.0074 | *Npw* | 1.758465 | 0.037 | *Trim10* | -1.65321 | 0.0056 |
| *Nmb* | -1.86515 | 0.0026 | *Lrp2* | 1.668749 | 0.0118 | *Steap1* | 1.627907 | 0.0266 |
| *Smim32* | 1.864586 | 0.0096 | *Tagln* | -1.64991 | 0.0026 | *Il18r1* | 1.626486 | 0.0172 |
| *Ecm1* | -1.75846 | 0.0008 | *Lrrc9* | 1.529791 | 0.034 | *Myo3a* | -1.54983 | 0.0046 |
| *Zic4* | -1.75188 | 0.0046 | *Cbl* | -1.51526 | 0.0186 | *Fbxo43* | 1.53378 | 0.0164 |
| *Alkbh8* | -1.73714 | 0.0028 | *Arhgap28* | -1.50624 | 0.0246 | *Edn3* | -1.52287 | 0.0268 |
| *Ghdc* | 1.679592 | 0.0012 | *Smad6* | -1.48152 | 0.0044 | *Rgs22* | 1.487865 | 0.0272 |
| *Diaph3* | -1.62275 | 0.0168 | *Exoc3l2* | -1.47295 | 0.0204 | *Ncf2* | -1.45757 | 0.0096 |
| *Bmp3* | 1.585725 | 0.0018 | *Ctxnd1* | -1.45043 | 0.0164 | *Etfbkmt* | -1.44306 | 0.0066 |
| *Nmu* | 1.575957 | 0.0072 | *Gpr50* | 1.429156 | 0.0176 | *Trmt2b* | -1.43991 | 0.0272 |
| *Acta1* | -1.53146 | 0.044 | *Col1a1* | -1.42618 | 0.0312 | *Morn5* | 1.427706 | 0.027 |
| *Gpr50* | -1.51998 | 0.0384 | *Evpl* | -1.40366 | 0.0408 | *Siglec1* | -1.42272 | 0.017 |
| *Clrn1* | -1.51716 | 0.0364 | *Gas2l2* | 1.403227 | 0.045 | *Rac2* | -1.4084 | 0.0288 |
| *Krt77* | -1.46919 | 0.0246 | *Atp7b* | 1.367329 | 0.0006 | *Eln* | 1.391259 | 0.005 |
| *Irs4* | -1.45883 | 0.0054 | *Crtam* | 1.357569 | 0.0202 | *Jmjd4* | 1.387232 | 0.017 |
| *Isl1* | -1.43804 | 0.0234 | *Krtcap3* | 1.356831 | 0.0018 | *Ptgis* | -1.34655 | 0.0048 |
| *Slc7a14* | -1.43257 | 0.0136 | *Dock6* | -1.35372 | 0.0148 | *Atp8b1* | -1.3178 | 0.0154 |

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| Table 1. Summary of top highly differentially expressed genes across all regions analyzed. LH: lateral hypothalamus, DMH: dorsomedial hypothalamus, ARC: arcuate nucleus of the hypothalamus. log2FC: log2 fold change in expression between groups. Positive values indicate lower levels of transcript in Stressed subjects; negative values indicate higher levels in Stressed subjects. eFDR: enhanced false discovery rate, or permuted p-value. |